Amendments to the Claims:

Please amend the claims as follows:

1 through 5. (Cancelled)

6. (Currently Amended) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation providing means for improving functionality of the variant cellobiohydrolase with respect to the wild-type cellobiohydrolase. ~~said nucleic acid sequence comprising a linker region sequence having a length of from about 20 nucleotides to about 50 nucleotides located, between a catalytic domain and a cellulose binding domain (CBD).~~

7. (Currently Amended) The nucleic acid molecule of claim 6 wherein the ~~variant cellobiohydrolase is further defined as having enhanced thermostability~~ means for improving is selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) glycine at position 99;

(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;

(e) a cysteine at positions 197 and 370;

(f) a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(g) alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof;

(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and

(i) any combination of the mutations of (a), (b), (c), (d), (e), (f), (g), (h), wherein the positional reference is within an amino acid sequence encoding a native cellobiohydrolase I of SEQ ID NO: 5.

8. (Currently Amended) The nucleic acid molecule of claim 67 wherein the ~~variant cellobiohydrolase is further defined as an 1,4 β-cellobiohydrolase~~ means for improving comprises the proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof.

9. (Currently Amended) The nucleic acid molecule of claim 67 wherein the ~~wherein the cellobiohydrolase is further defined as having reduced end product inhibition.~~ means for improving comprises the helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof.

10. (Currently Amended) The nucleic acid ~~molecular~~ molecule of claim 67 wherein the ~~linker region sequence has a length of about 24 nucleotides~~ means for improving comprises the glycine at position 99.

11. (Currently Amended) A method for mutating a nucleic acid encoding a wild type cellobiohydrolase of SEQ ID NO: 5, the method comprising:

mutating the wild type cellobiohydrolase with a mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) glycine at position 99;

(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;

(e) a cysteine at positions 197 and 370;

(f) a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(g) alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof;

(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and

(i) any combination of the mutations of (a), (b), (c), (d), (e), (f), (g), (h), wherein the position al reference is within an amino acid sequence encoding a native cellobiohydrolase I of SEQ ID NO: 5.

~~making an active exoglucanase in a eukaryotic heterologous host, the method comprising reducing glycosylation of the exoglucanase, wherein reducing comprises~~

~~replacing an amino acid that has an N-glycosylation site with a replacement residue not having such a site~~

12. (Currently Amended) The method of claim 11, wherein the ~~amino acid that has the N-glycosylation site includes asparagine together with surrounding amino acid residues as encoded by at least one of SEQ ID NO. 20, 21, and 22, and the replacement residue includes alanine together with surrounding amino acid residues as encoded by at least one of SEQ ID, NO. 83, 85, and 87~~ mutation comprises the non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

13. (Currently Amended) The method of claims 11, wherein the step of mutating ~~replacing~~ comprises site-directed mutagenesis.

14. (Currently amended) The method of claim 11, further comprising a step of shortening a linker region sequence being shortened with respect to SEQ ID NO: 2 to provide comprises a linker region sequence having a length of from about 20 nucleotides to about 50 nucleotides located, between a catalytic domain and a cellulose binding domain (CBD) of SEQ ID NO: 5 ~~wherein the exoglucanase comprises a cellobiohydrolase.~~

15. (Previously presented) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 20.

16. (Previously presented) An exoglucanase, comprising the sequence change encoded by SEQ ID NO: 21.

17. (Cancelled)

18. (Currently Amended) An exoglucanase composition, comprising a combination of exoglucanases selected from the group consisting of exoglucanases defined by claims 15 and 16~~,16, and 17~~.

19. (New) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof.

20. (New) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the cysteine at positions 197 and 370.

21. (New) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

22. (New) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof.

23. (New) The nucleic acid molecule of claim 7 wherein the means for enhancing thermostability comprises the alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof.

24. (New) The nucleic acid molecule of claim 7 wherein the means for improving comprises means for enhancing thermostability.

25. (New) The nucleic acid molecule of claim 1, wherein the variant celllobiohydrolase comprises a linker region sequence having a length of from about 20 nucleotides to about 50 nucleotides located, between a catalytic domain and a cellulose binding domain (CBD), the linker region sequence being shortened with respect to SEQ ID NO: 2.

26. (New) A nucleic acid molecule having a nucleic acid sequence encoding a variant cellobiohydrolase that is mutated with respect to a wild-type cellobiohydrolase of SEQ ID NO: 5, the mutation selected from the group consisting of:

(a) proline substituted at a position selected from the group consisting of position 8, 27, 43, 75, 94, 190, 195, 287, 299, 312, 315, 359, 398, 401, 414, 431, 433, and any combination thereof;

(b) a helix-capping mutation defined as an arginine or aspartic acid residue is substituted at a position selected from the group consisting of position 64, 337, 327, 405, 410 and any combination thereof;

(c) glycine at position 99;

(d) a deletion from the group consisting of position 99-101, position 278-279, and position 387, and any combination thereof;

(e) a cysteine at positions 197 and 370;

(f) a non-glycosyl accepting amino acid residue in place of an N-glycosylation site amino acid residue at a position selected from the group consisting of position 45, 270, 384 and any combination thereof,

(g) alanine at a position selected from the group consisting of position 45, 270, 384 and any combination thereof;

(h) alanine at a position selected from the group consisting of position 252, 294, 338, 267, 385, and any combination thereof; and

(i) any combination of the mutations of (a), (b), (c), (d), (e), (f), (g), (h), wherein the position al reference is within an amino acid sequence encoding a native cellobiohydrolase I of SEQ ID NO: 5.